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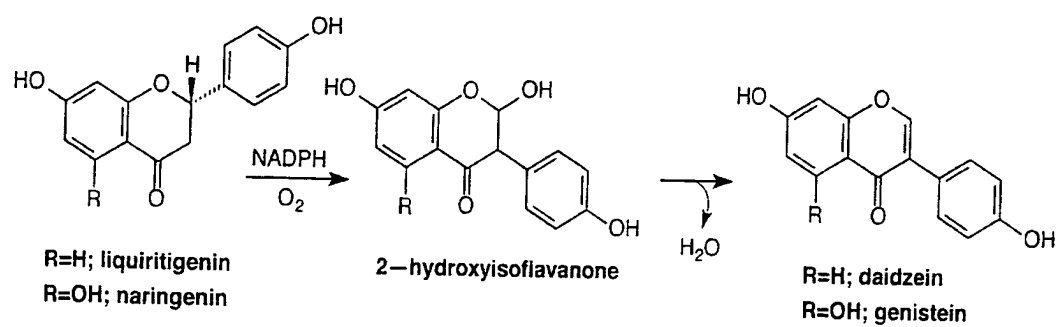


Fig. 1

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101 CACTGCAAAA TCAAAAGCAC TTCGCCATCT CCCAAACCCA CCAAGCCCCAA
151 AGCCTCGTCT TCCCTTCATA GGACACCTTC ATCTCTTAAA AGACAAACTT
201 CTCCACTACG CACTCATCGA CCTCTCCAAA AAACATGGTC CCTTATTCTC
251 TCTCTACTTT GGCTCCATGC CAACCGTTGT TGCCTCCACA CCAGAATTGT
301 TCAAGCTCTT CCTCCAAACG CACGAGGCAA CTTCTTCAA CACAAGGTTC
351 CAAACCTCAG CCATAAGACG CCTCACCTAT GATAGCTCAG TGGCCATGGT
401 TCCCTTCGGA CCTTACTGGA AGTTCGTGAG GAAGCTCATC ATGAACGACC
451 TTCTCAACGC CACCACTGTA AACAAGTTGA GGCCTTTGAG GACCCAACAG
501 ATCCGCAAGT TCCTTAGGGT TATGGCCCAA GGCGCAGAGG CACAGAAGCC
551 CCTTGACTTG ACCGAGGAGC TTCTGAAATG GACCAACAGC ACCATCTCCA
601 TGATGATGCT CGGCGAGGCT GAGGAGATCA GAGACATCGC TCGCGAGGTT
651 CTTAAGATCT TTGGGAATA CAGCCTCACT GACTTCATCT GGCCATTGAA
701 GCATCTCAAG GTTGGAAAGT ATGAGAAGAG GATCGACGAC ATCTTGAACA
751 AGTTCGACCC TGTCGTTGAA AGGGTCATCA AGAAGCGCCG TGAGATCGTG
801 AGGAGGAGAA AGAACGGAGA GGTGTTGAG GGTGAGGTCA GCGGGGTTTT
851 CCTTGACACT TTGCTTGAAT TCGCTGAGGA TGAGACCATG GAGATCAAAA
901 TCACCAAGGA CCACATCAAG GGTCTTGTG TCGACTTTTT CTCGGCAGGA
951 ACAGACTCCA CAGCGGTGGC AACAGAGTGG GCATTGGCAG AACTCATCAA
1001 CAATCCTAAG GTGTTGAAA AGGCTCGTGA GGAGGTCTAC AGTGTGTGG
1051 GAAAGGACAG ACTTGTGGAC GAAGTTGACA CTCAAACCT TCCTTACATT
1101 AGAGCAATCG TGAAGGAGAC ATTCCGCATG CACCCGCCAC TCCAGTGGT
1151 CAAAAGAAAG TGCACAGAAG AGTGTGAGAT TAATGGATAT GTGATCCCAG
1201 AGGGAGCATT GATTCTCTTC AATGTATGGC AAGTAGGAAG AGACCCAAA
1251 TACTGGGACA GACCATCGGA GTTCCGTCCT GAGAGGTTC TAGAGACAGG
1301 GGCTGAAGGG GAAGCAGGGC CTCTTGATCT TAGGGGACAA CATTTTCAAC
1351 TTCTCCCAT TGGGTCTGGG AGGAGAATGT GCCCTGGAGT CAATCTGGCT
1401 ACTTCGGGAA TGGCAACACT TCTTGACATCT CTTATTCAGT GCTTCGACTT
1451 GCAAGTGCTG GGTCCACAAG GACAGATATT GAAGGTGGT GACGCCAAG
1501 TTAGCATGGA AGAGAGAGCC GGCCTCACTG TTCCAAGGGC ACATAGTCTT
1551 GTCTGTGTT CACTTGCAAG GATCGGCGTT GCATCTAAAC TCCTTTCTTA
1601 ATTAAGATCA TCGTCATCAT CATCATATGT AATATTTACT TTTTGTGTGT
1651 TGATAATCAT CATTTCAATA AGGTCTCATT CATCTACTTT TTATGAAGTA
1701 TATAAGCCCT TCCATGC

Fig. 2

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1 CAACACCTAA GAGTAACTAA TAAGAACTTT CTTTCTACTT CTTAGTATAC
 51 TTAACAACCTT AAGTAAATAT ACTACAAAGA AGCTATACAC CATGTTGGTG
 101 GAACCTGCGAG TTAGCTCTATT GCTCATTGCT CTCTTCTTAC ACTTGCGTCC
 151 AACACCTACT GCAAAATCAA AGGCTCTTCG CCACCTTCCA AATCCACCAA
 201 GCCCTAAACC ACGTCTTCCA TTCATAGGTC ATCTTCACCT TTTGGATAAC
 251 CCACTTCTTC ACCACACTCT TATCAAGTTA GGAAAGCGTT ATGGCCCTTT
 301 GTACACTCTT TACTTTGGTT CCATGCCTAC CGTTGTTGCA TCCACTCCTG
 351 ACTTGTTTAA ACTTTTCCTT CAAACCCATG AAGCTACTTC CTTTAACACA
 401 AGATTCCAAA CCTCTGCTAT TAGTCGTCTT ACCTATGACA ACTCTGTTGC
 451 TATGGTTCCA TTTGCACCTT ATTGGAAGTT TATTAGAAAG CTTATCATGA
 501 ACGACTTGCT CAACGCCACC ACTGTTAACA AATTGAGGCC ATTGAGGAGC
 551 CGAGAAATCC TTAAGGTTCT TAAGGTCATG GCTAATAGTG CTGAAACTCA
 601 ACAGCCACTT GATGTCCTG AGGAGCTTCT CAAGTGGACA AACAGCACAA
 651 TCTCTACCAT GATGTTGGGT GAGGCCGAAG AGGTTAGAGA TATTGCTCGT
 701 GATGTTCTTA AGATCTTTGG AGAATATAGT GTTACAAACT TTATTTGGCC
 751 TTTGAACAAG TTTAAGTTTG GAAACTATGA TAAGAGAACT GAGGAGATTT
 801 TCAATAAGTA TGATCCTATC ATTGAAAAGG TTATCAAGAA ACGACAAGAG
 851 ATTGTGAACA AAAGAAAAAA TGGAGAAATC GTAGAAGGCG AGCAGAATGT
 901 TGTTTTTCTT GACACTTTGC TTGAATTTGC ACAAGATGAG ACCATGGAGA
 951 TCAAAATTAC AAAGGAACAA ATCAAGGGTC TTGTTGTGGA TTTTTTCTCT
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 1251 TTCCAGAAGG AGCACTAATA CTTTTCAATG TCTGGGCAGT GGAAGAGAC
 1301 CCAAAATATT GGGTAAAGCC ATTGGAATTT CGTCCAGAGA GGTTCATAGA
 1351 AAATGTTGGT GAAGGTGAAG CAGCTTCAAT TGATCTTAGG GGTCAACATT
 1401 TCACACTTCT ACCATTTGGG TCTGGAAGAA GGATGTGTCC TGGAGTCAAT
 1451 TTGGCTACTG CAGGAATGGC CACAATGATT GCATCTATTA TCCAATGCTT
 1501 CGATCTCCAA GTACCTGGTC AACATGGAGA AATATTGAAT GGTGATTATG
 1551 CTAAGGTTAG CATGGAAGAG AGACCTGGTC TCACAGTTCC AAGGGCACAT
 1601 AATCTCATGT GTGTTCTCTT TGCAAGAGCT GGTGTGCGAG ATAACTTCT
 1651 TTCCTCCTAA AATATCTTGA GAGGATGAAT CACCAACATA TAGCCTCTCT
 1701 TTGGTACTAC AAAATTATGA TGTAAATTTT TTATTTTTTC TGTCACAAAG
 1751 GAAGTGTGT AACTTGTAAT TGCATACAAA ATCTATAAAT TTTATCATCC
 1801 TATTCATTAT T

Fig. 4

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mtIFS 1 MLVELAVTLLLLIALFLHLRPTPTAKSKALRHLNPPSPKPRLPFIGHLHL 50
 ||.|||. ||.:||||||||||||||||||||||||||||||||
CYP93C1v2 1 MLELALGLLVLALFLHLRPTPTAKSKALRHLNPPSPKPRLPFIGHLHL 50
 51 LDNPLLHHTLIKLGKRYGPLYTLYFGSMPTVVASTPDLFKLFLQTHEATS 100
 | . |||: || | |:|||: . |||||||||||||||: |||||||
 51 LKDKLLHYALIDLKSKHGPLFSLYFGSMPTVVASTPELFLKLFLQTHEATS 100
 101 FNTRFQTS AISRLTYDNSVAMVPFAPYWK FIRKLIMNDLLNATTVNKL RP 150
 ||||| ||||| ||||| |||||: ||||| |||||
 101 FNTRFQTS AIRRLTYDSSVAMVPFGPYWK FVRKLIMNDLLNATTVNKL RP 150
 151 LRSREILKVLKVMANSAETQQPLDVTEELLKWTNSTISTMMLGEAEV RD 200
 ||.: || | |: || | | . ||||| ||||| |||||: ||
 151 LRTQQIRKFLRVMAQGAQAQKPLDLTEELLKWTNSTISMMLGEAEI RD 200
 201 IARDVLKIFGEYSVTNFIWPLNKFKEGNYDKRTEEIFNKYDPIIEKVIK 250
 |||: ||||| ||||| . ||||| || | |: || | |: |||: |||
 201 IAREVLKIFGEYSLTDFIWPLKHLKVGKYEKRIDDILNKFDPVVERVIK 250
 251 RQEIVNKRKNGEIVEGEQNVVFLDTLLEFAQDETMEIKITKEQIKGLVVD 300
 |. ||| : |||||: ||||| . ||||| |||||: |||||: |||||
 251 RREIVRRRKNGEVVEGEVSGVFLDTLLEFAEDETMEIKITKDHIKGLVVD 300
 301 FFSAGTDSTAVSTEWTLSELINNPRVLKKAREEIDS SVVGKDRLVDES DVQ 350
 ||||| ||||| . ||| |. |||||: ||. |||||: ||||| ||||| | |
 301 FFSAGTDSTAVATEWALAE LINNPKVLEKAREEVYSVVGKDRLVDEVD TQ 350
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 351 NLPYIRAIVKETFRMHPPPLPVVKRKCTEECEINGYVIPEGALILFNWQV 400
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 401 GRDPKYWDRPSEFRPERFLETGAEGEAGPLDLRGQHFQLLPFGSGRRMCP 450
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 451 GVNLATSGMATLLASLIQC FDLQVLGPQGQILKGGDAKVSMEERAGLTVP 500
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 501 RAHSLVCVPLARIGVASKLLS 521

Fig. 5

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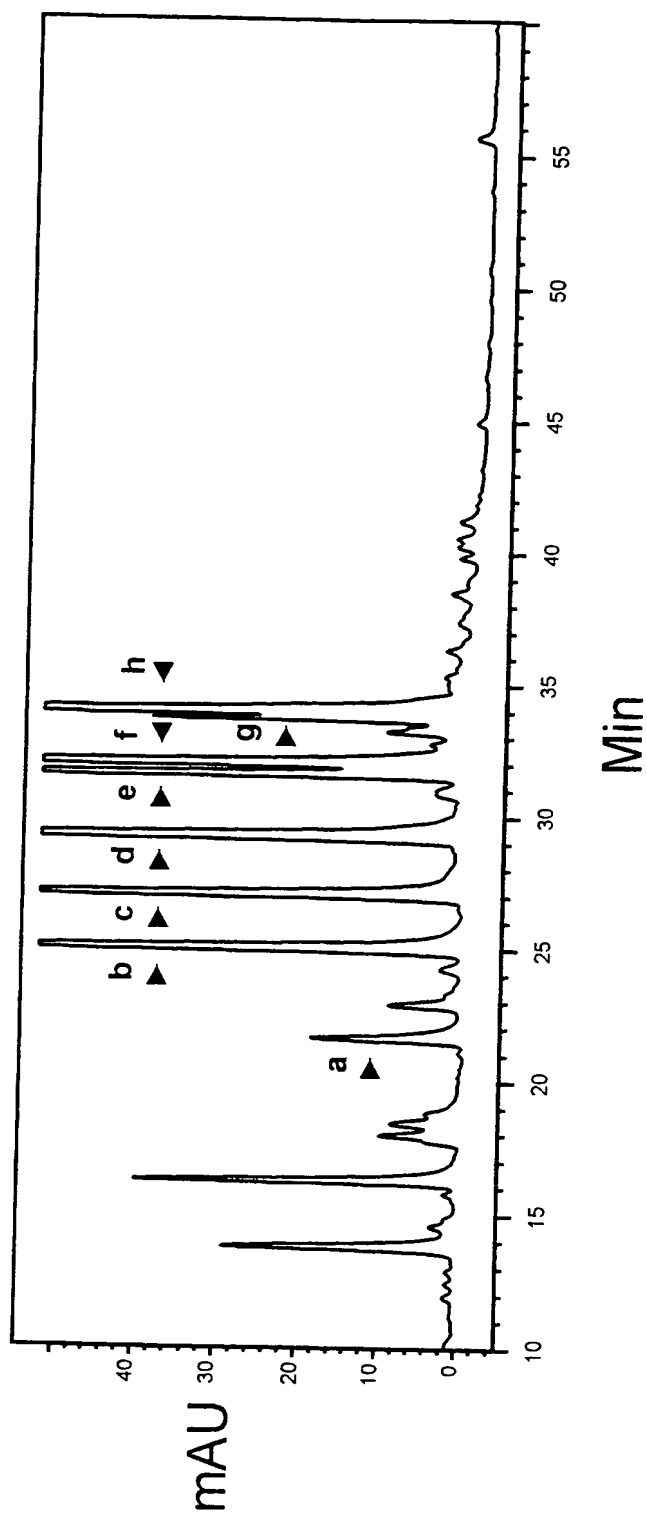


Fig. 6A

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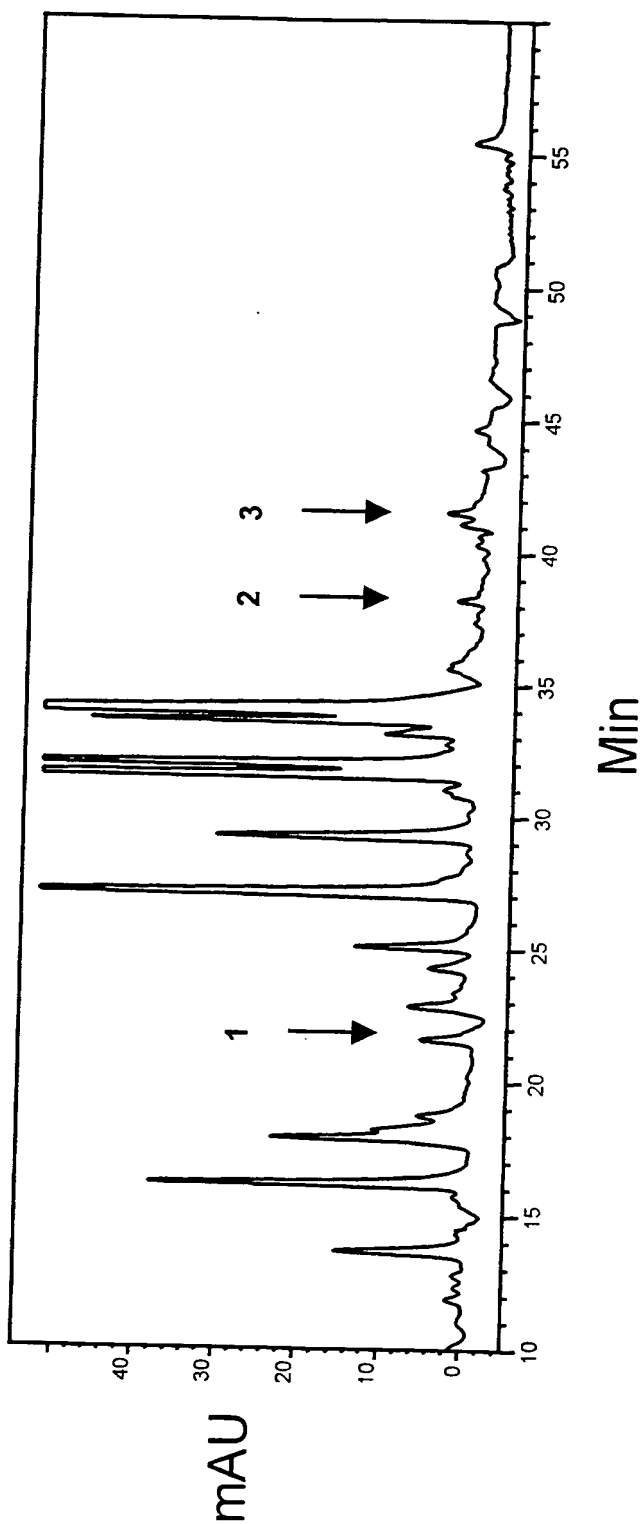


Fig. 6B

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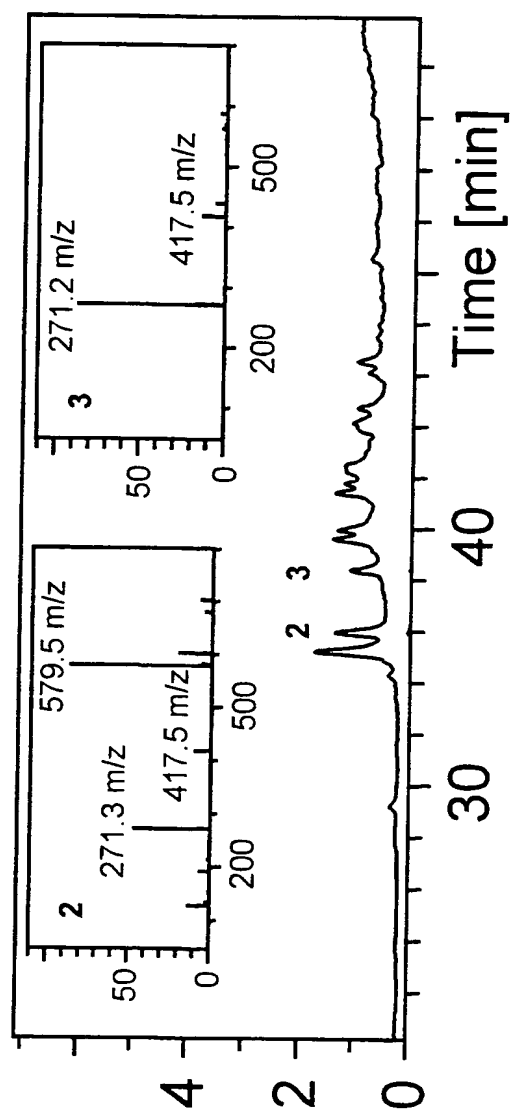


Fig. 6C

FIG. 6C

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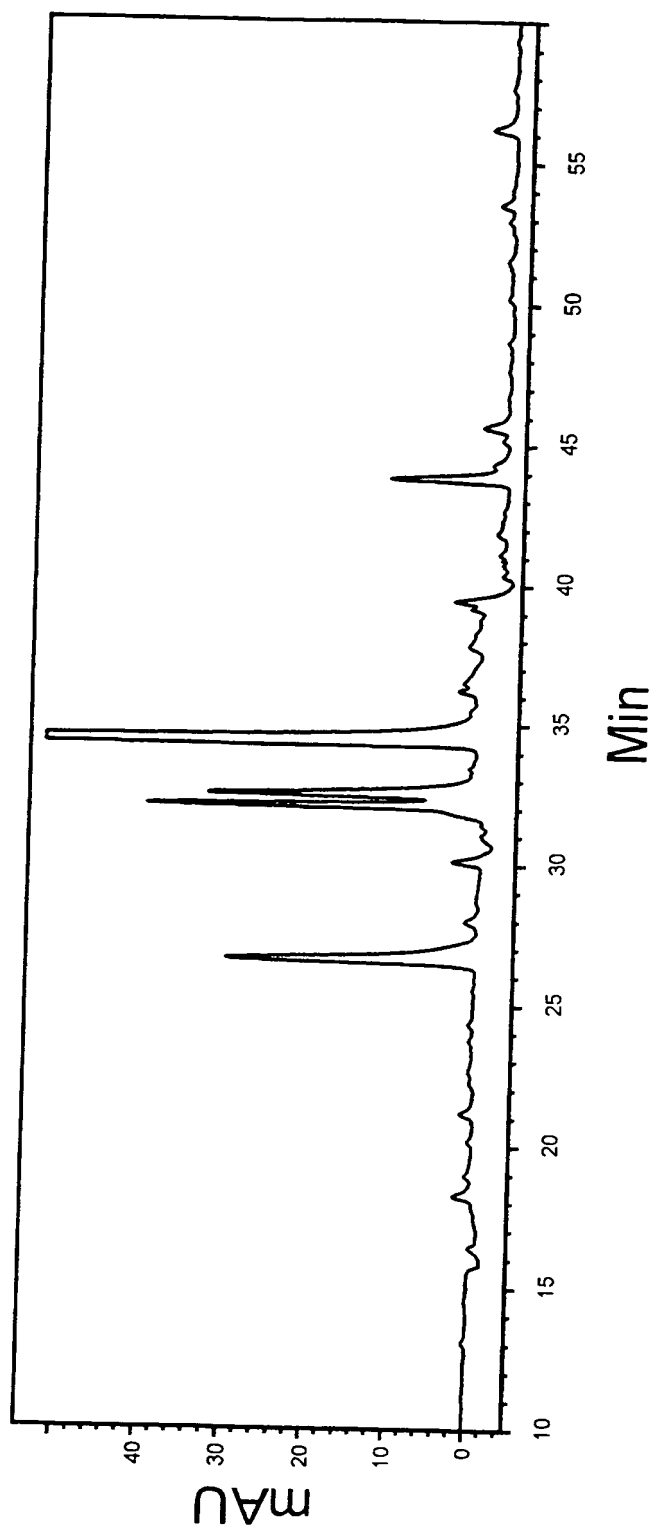


Fig. 7A

Figure 7A

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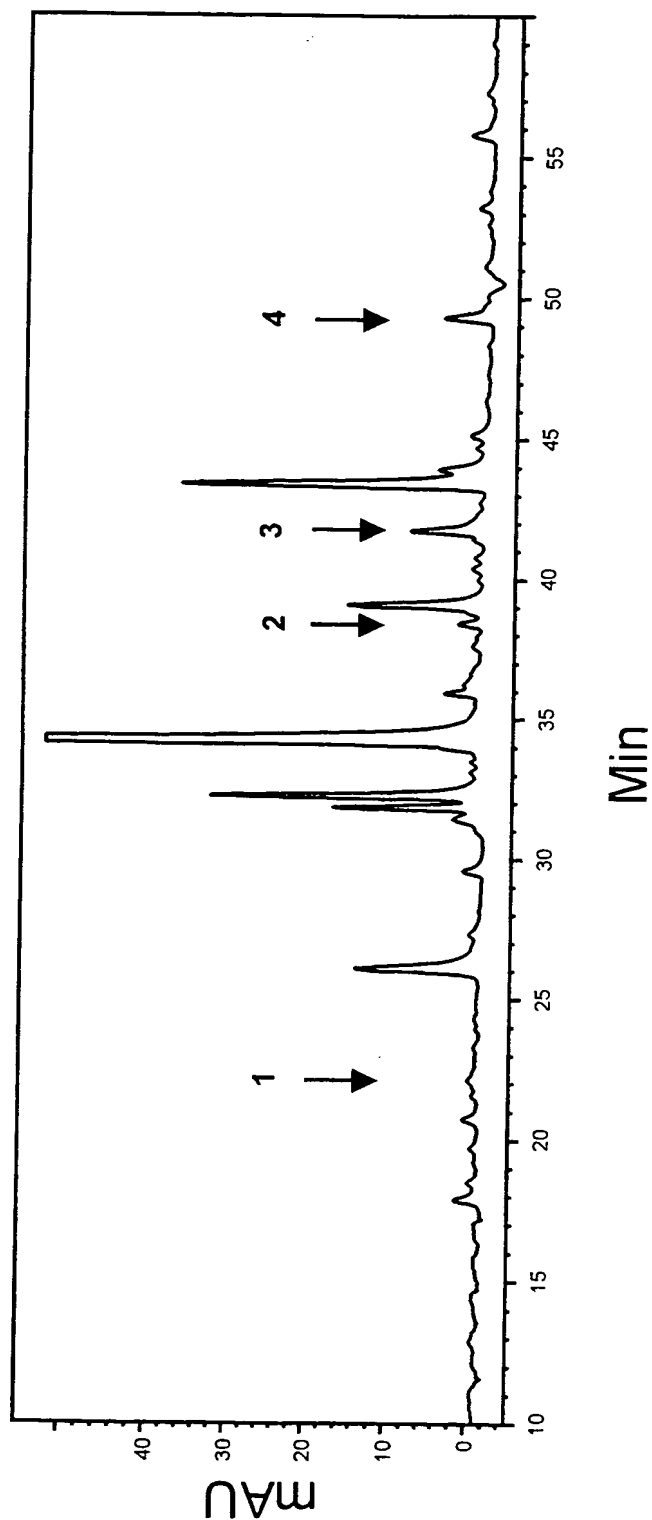


Fig. 7B

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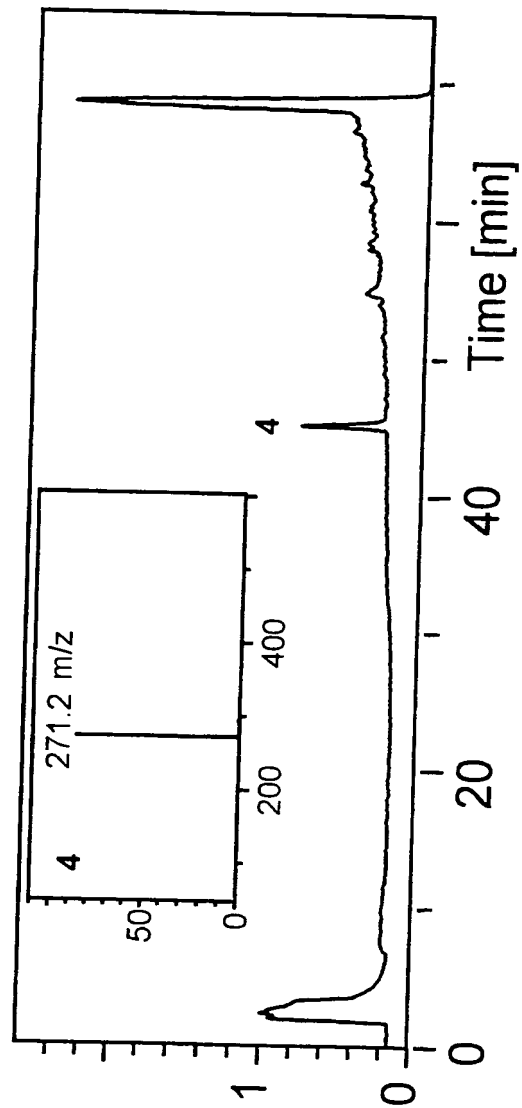


Fig. 7C

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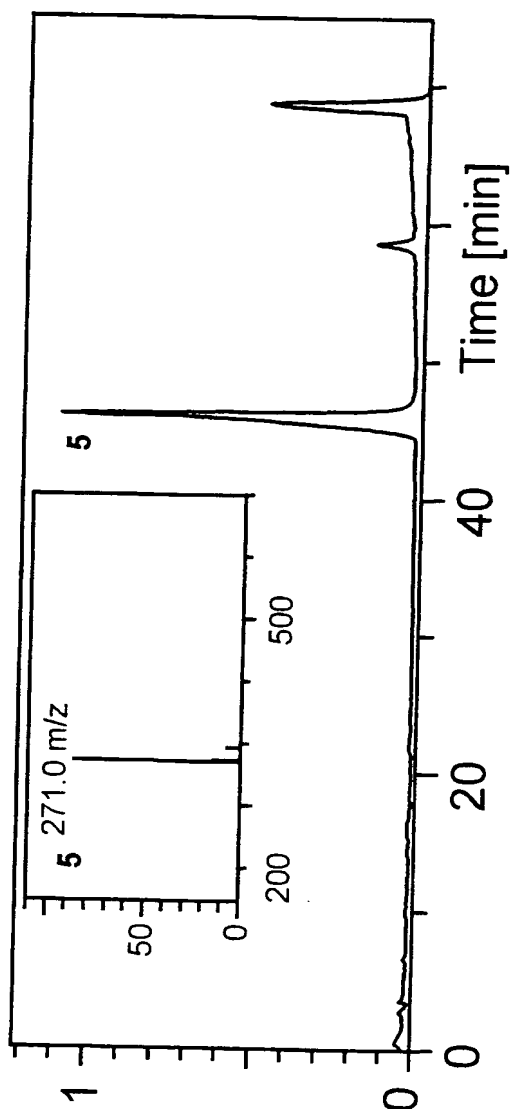


Fig. 7D

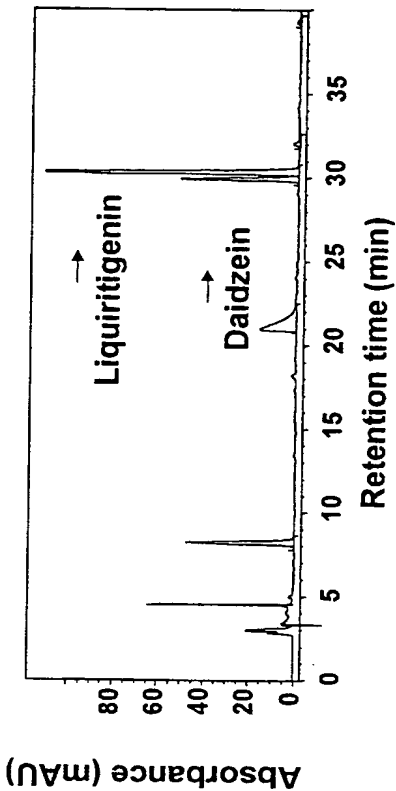


Fig. 8A

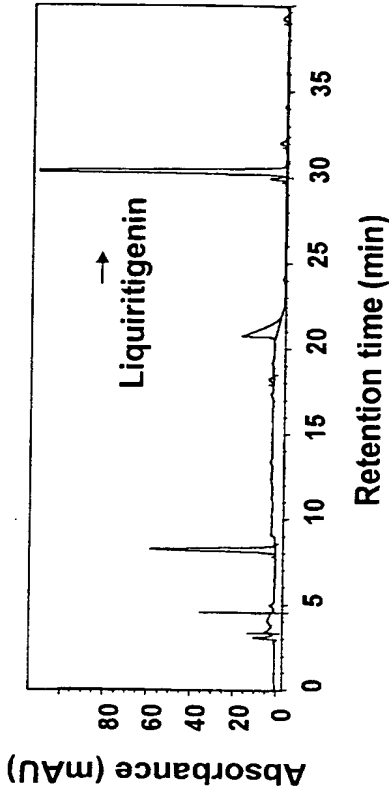


Fig. 8B

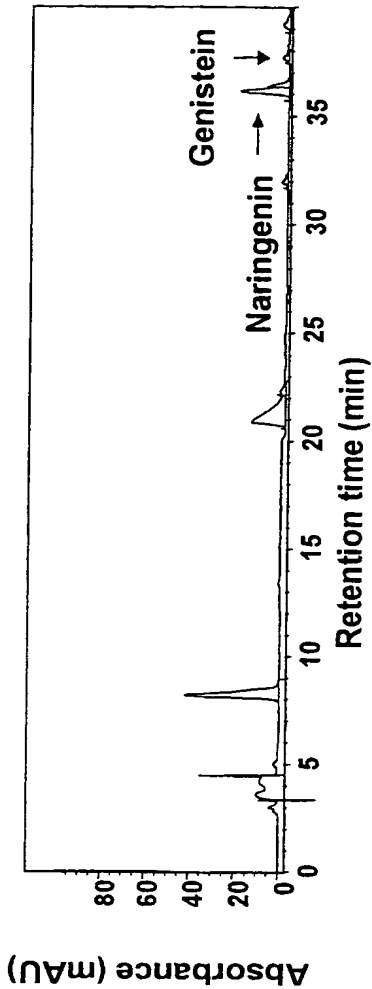


Fig. 8C

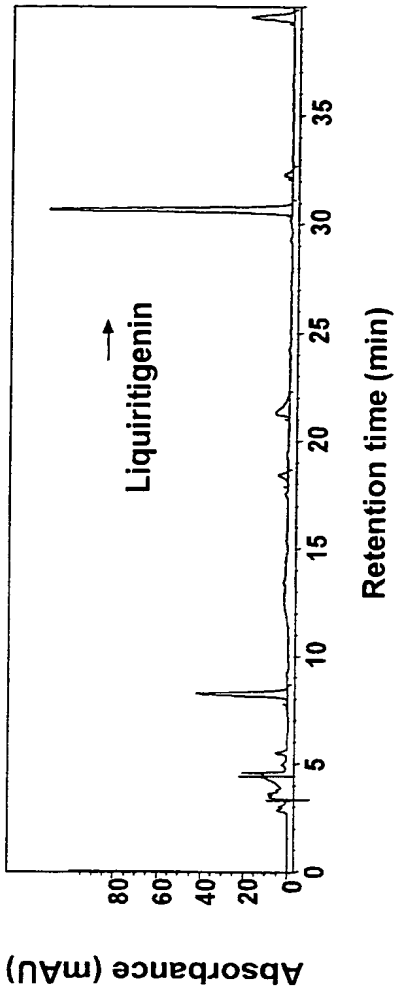


Fig. 8D

Fig. 9A

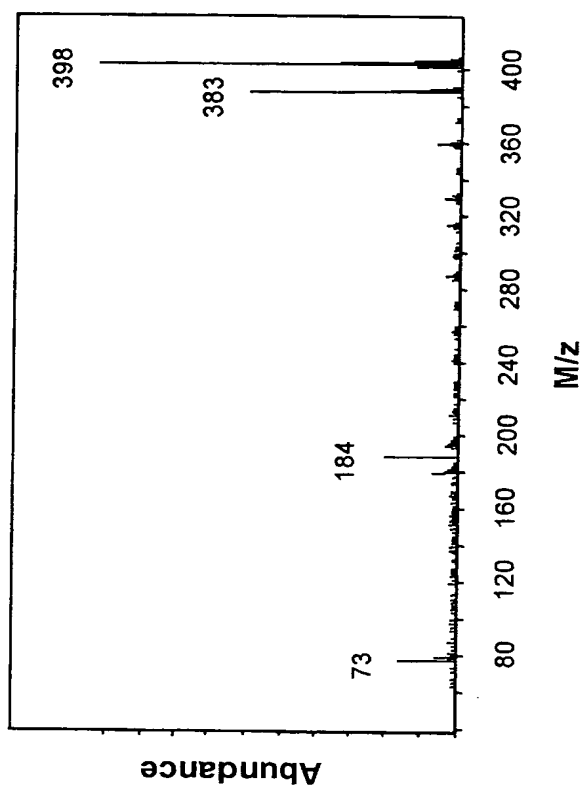


Fig. 9B

